

SEQUENCE LISTING



<110> Quertermous, Thomas
Hogan, Brigid
Snodgrass, Ralph H
Zupancic, Thomas J

<120> Antibodies Binding to Polypeptides Encoded by Developmentally-Regulated Endothelial Cell Locus-1

<130> 238/300

<140> US 09/237,981

<141> 1999-01-25

<150> US 08/659,235

<151> 1996-06-05

<160> 31

<170> PatentIn version 3.1

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Xaa	Ala	Lys	Asp	Phe	Gly	Asp	Val	Leu	Phe	Val	Gly	Ser	Tyr	Lys	Leu
			20					25					30		

Ala Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys
35 40 45

Gln Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His
50 55 60

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20 25 30

Ala Tyr Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg
35 40 45

Thr Gly Ser Ser Lys Val Phe Gln Gly Asn Leu Asp Asn Asn Ser His
50 55 60

Lys Lys Asn Ile Phe Glu Lys Pro Phe Met Ala Arg Tyr Val Arg Val
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20 25 30

His Tyr Ser Glu Gln Gly Val Glu Trp Lys Pro Tyr Arg Leu Lys Ser
35 40 45

Ser Met Val Asp Lys Ile Phe Glu Gly Asn Thr Asn Thr Lys Gly His
50 55 60

Val Lys Asn Phe Phe Asn Pro Pro Ile Ile Ser Arg Phe Ile Arg Val

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		20						25					30		

Ser	Ser	Ser	Gln	Asp	Gly	His	His	Trp	Thr	Xaa	Xaa	Gln	Ile	Leu	Tyr
		35					40					45			

Asn	Gly	Lys	Val	Lys	Val	Phe	Gln	Gly	Asn	Gln	Asp	Ser	Ser	Thr	Pro
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Asp Ile Ser Ser Asn Gly Glu Asp Trp Ile Xaa Xaa Thr Leu Lys Gly
35 40 45

Asp Asn Lys His Leu Val Phe Thr Gly Asn Thr Asp Ala Thr Asp Val
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Val Tyr Arg Pro Phe Ser Lys Pro Val Ile Thr Arg Phe Val Arg Leu
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Gly Tyr Ser Asn Asn Gly Thr Glu Trp Gly Met Ile Met Asp Ser Ser
35 40 45

Lys Asn Lys Pro Lys Thr Phe Glu Gly Asn Thr Asn Tyr Asp Thr Pro
50 55 60

Glu Leu Arg Thr Phe Xaa Ala His Ile Thr Thr Gly Phe Ile Arg Ile
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 20 25 30

Arg Tyr Ser Leu Asp Asn Val Ser Trp Phe Xaa Xaa Xaa Xaa Xaa Glu
 35 40 45

Tyr Arg Asp Gly Ala Ala Ile Thr Gly Val Thr Asp Arg Asn Thr Val
 50 55 60

Val Asn His Phe Phe Asp Thr Pro Ile Arg Ala Arg Ser Ile Ala Ile
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His Pro Leu Thr Xaa
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 20 25 30

Xaa Tyr Ser Xaa Asp Gly Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45

Xaa Xaa Lys Xaa Lys Val Phe Xaa Gly Asn Thr Asp Xaa Xaa Thr Xaa
 50 55 60

Xaa Xaa Asn Xaa Phe Xaa Xaa Pro Ile Xaa Xaa Arg Phe Ile Arg Xaa
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Xaa Pro Xaa Xaa Xaa
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cgcccgtag aagggatc atg aag cac ttg gta gca gcc tgg ctt ttg gtt	651
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Gly Leu Ser Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn	
15 20 25	
ccg aac ccc tgt gaa aat ggt ggc atc tgt ctg tca gga ctg gct gat	747
Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp	
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gat tcc ttt tcc tgt gag tgt cca gaa ggc ttc gca ggt ccg aac tgc	795
Asp Ser Phe Ser Cys Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys	
45 50 55	
tct agt gtt gtg gag gtt gca tca gat gaa gaa aag cct act tca gca	843
Ser Ser Val Val Glu Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala	
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ggt ccc tgc atc cct aac cca tgc cat aac gga gga acc tgt gag ata	891
Gly Pro Cys Ile Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile	
80 85 90	
agc gaa gcc tat cga gga gac aca ttc ata ggc tat gtt tgt aaa tgt	939

Ser Glu Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys
 95 100 105

cct cgg gga ttt aat ggg att cac tgt cag cac aat ata aat gaa tgt 987
 Pro Arg Gly Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys
 110 115 120

gaa gct gag cct tgc aga aat ggc gga ata tgt acc gac ctt gtt gct 1035
 Glu Ala Glu Pro Cys Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala
 125 130 135

aac tac tct tgt gaa tgc cca gga gaa ttt atg gga cga aat tgt caa 1083
 Asn Tyr Ser Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln
 140 145 150 155

tat aaa tgc tct ggg cac ttg gga atc gaa ggt ggg atc ata tct aat 1131
 Tyr Lys Cys Ser Gly His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn
 160 165 170

cag caa atc aca gct tca tct aat cac cga gct ctt ttt gga ctc cag 1179
 Gln Gln Ile Thr Ala Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln
 175 180 185

aag tgg tat ccc tac tat gct cga ctt aat aag aag ggc ctt ata aat 1227
 Lys Trp Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn
 190 195 200

gcc tgg aca gct gct gaa aat gac aga tgg cca tgg att cag ata aat 1275
 Ala Trp Thr Ala Ala Glu Asn Asp Arg Trp Pro Trp Ile Gln Ile Asn
 205 210 215

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 220 225 230 235

agg att gga agc cca gag tac ata aaa tcc tac aaa att gcc tac agc 1371
 Arg Ile Gly Ser Pro Glu Tyr Ile Lys Ser Tyr Lys Ile Ala Tyr Ser
 240 245 250

aat gac ggg aag acc tgg gca atg tac aaa gta aaa ggc acc aat gaa 1419
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 255 260 265

gag atg gtc ttt cgt gga aat gtt gat aac aac aca cca tat gct aat 1467
 Glu Met Val Phe Arg Gly Asn Val Asp Asn Asn Thr Pro Tyr Ala Asn
 270 275 280

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Ser	Phe	Thr	Pro	Pro	Ile	Lys	Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Gln	
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ctc	tca	ggc	tgt	tca	gaa	cct	ttg	ggg	atg	aaa	tca	ggg	cat	ata	caa	1611
Leu	Ser	Gly	Cys	Ser	Glu	Pro	Leu	Gly	Met	Lys	Ser	Gly	His	Ile	Gln	
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gac	tac	cag	atc	act	gcc	tcc	agc	gtc	ttc	aga	aca	ctc	aac	atg	gac	1659
Asp	Tyr	Gln	Ile	Thr	Ala	Ser	Ser	Val	Phe	Arg	Thr	Leu	Asn	Met	Asp	
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Lys	Asn	Val	Ile	Asp	Pro	Pro	Ile	Tyr	Ala	Arg	Phe	Ile	Arg	Ile	Leu	
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Pro	Trp	Ser	Trp	Tyr	Gly	Arg	Ile	Thr	Leu	Arg	Ser	Glu	Leu	Leu	Gly	
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Cys Ala Glu Glu Glu
480

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Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro Cys Glu
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35 40 45

Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val Val Glu
50 55 60

Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys Ile Pro
65 70 75 80

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
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Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
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Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu Pro Cys

115	120	125
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Tyr Ala Arg Leu Asn Lys Lys Gly	Leu Ile Asn Ala Trp Thr Ala Ala	
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Glu Asn Asp Arg Trp Pro Trp Ile	Gln Ile Asn Leu Gln Arg Lys Met	
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Glu Tyr Ile Lys Ser Tyr Lys Ile Ala	Tyr Ser Asn Asp Gly Lys Thr	
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Trp Ala Met Tyr Lys Val Lys Gly Thr	Asn Glu Glu Met Val Phe Arg	
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Gly Asn Val Asp Asn Asn Thr Pro Tyr Ala	Asn Ser Phe Thr Pro Pro	
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Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln	Ile Cys Arg Arg His	
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Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp Thr
                355                360                365

Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu Val
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Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe Gly
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His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp Gly
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Glu His Trp Met Val His Gln Asp Glu Lys Gln Arg Lys Asp Lys Val
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Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp
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Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu Pro Trp Ser Trp Tyr
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caggtggatc ttcttgttcc aaccaaagtg actggcatca ttacacaagg agctaaagat      1380
tttggtcatg tacagtttgt tggtcctac aaactggctt acagcaatga tggagaacac      1440

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tggactgtat accaggatga aaagcaaaga aaagataagg ttttccaggg aaattttgac 1500
aatgacactc acagaaaaaa tgtcatcgac cctcccatct atgcacgaca cataagaatc 1560
cttccttggt cctggtacgg gaggatcaca ttggcgtcag agctgctggg ctgcacagag 1620
gaggaatgag gggaggctac atttcacaac cgtcttcctt atttgggtaa aagtatctcc 1680
atggaatgaa ctgtgtaaaa tctgtaggaa actgaatggg tttttttttt ttcatgaaaa 1740
agtgggtcaaa ttatggtagg caactaacgg tgtttttacc 1780

```

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<210> 12
<211> 14
<212> PRT
<213> Homo sapiens

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<400> 12
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Ser Pro Leu Ser Pro Ser Pro Arg Ile Cys Leu Thr Lys Arg
1           5           10

```

```

<210> 13
<211> 6
<212> PRT
<213> Homo sapiens

```

```
<400> 13
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```

Gly Lys Arg Thr Ser Ser
1           5

```

```

<210> 14
<211> 513
<212> PRT
<213> Homo sapiens

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```
<400> 14
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```

Gly Arg Ser Leu Leu Leu Pro Cys Ala Ala Thr Ser Ala Thr Leu Pro
1           5           10           15

```

```
Ser Ala Thr Thr Pro Asp Gln Pro Gly Ser Arg Pro Gly Asp Gly Ile
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20										25					30															
Met	Lys	Arg	Ser	Val	Ala	Val	Trp	Leu	Leu	Val	Gly	Leu	Ser	Leu	Gly															
		35					40					45																		
Val	Pro	Gln	Phe	Gly	Lys	Gly	Asp	Ile	Cys	Asp	Pro	Asn	Pro	Cys	Glu															
	50					55					60																			
Asn	Gly	Gly	Ile	Cys	Leu	Pro	Gly	Leu	Ala	Val	Gly	Ser	Phe	Ser	Cys															
65					70					75					80															
Glu	Cys	Pro	Asp	Gly	Phe	Thr	Asp	Pro	Asn	Cys	Ser	Ser	Val	Val	Glu															
				85					90					95																
Val	Ala	Ser	Asp	Glu	Glu	Glu	Pro	Thr	Ser	Ala	Gly	Pro	Cys	Thr	Pro															
			100					105					110																	
Asn	Pro	Cys	His	Asn	Gly	Gly	Thr	Cys	Glu	Ile	Ser	Glu	Ala	Tyr	Arg															
		115					120					125																		
Gly	Asp	Thr	Phe	Ile	Gly	Tyr	Val	Cys	Lys	Cys	Pro	Arg	Gly	Phe	Asn															
	130					135					140																			
Gly	Ile	His	Cys	Gln	His	Asn	Ile	Asn	Glu	Cys	Glu	Val	Glu	Pro	Cys															
145					150					155					160															
Lys	Asn	Gly	Gly	Ile	Cys	Thr	Asp	Leu	Val	Ala	Asn	Tyr	Ser	Cys	Glu															
				165					170					175																
Cys	Pro	Gly	Glu	Phe	Met	Gly	Arg	Asn	Cys	Gln	Tyr	Lys	Cys	Ser	Gly															
			180					185					190																	
Pro	Leu	Gly	Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn	Gln	Gln	Ile	Thr	Ala															
		195					200					205																		
Ser	Ser	Thr	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln	Lys	Trp	Tyr	Pro	Tyr															

210	215	220
Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala		
225	230	235 240
Glu Asn Asp Arg Trp Lys Arg Trp Ile Gln Ile Asn Leu Gln Arg Lys		
	245	250 255
Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser		
	260	265 270
Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys		
	275	280 285
Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Asp Met Val Phe		
	290	295 300
Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro		
305	310	315 320
Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val Cys Arg Arg		
	325	330 335
His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys		
	340	345 350
Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile		
	355	360 365
Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp		
	370	375 380
Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp		
385	390	395 400
Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu		

405

410

415

Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe
 420 425 430

Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp
 435 440 445

Gly Glu His Trp Thr Val Tyr Gln Asp Glu Lys Gln Arg Lys Asp Lys
 450 455 460

Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile
 465 470 475 480

Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp
 485 490 495

Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu
 500 505 510

Glu

<210> 15
 <211> 19
 <212> PRT
 <213> Homo sapiens

<400> 15

Gly Glu Ala Thr Phe His Asn Arg Leu Pro Tyr Leu Gly Lys Ser Ile
 1 5 10 15

Ser Met Glu

<210> 16
 <211> 9

<212> PRT
 <213> Homo sapiens

<400> 16

Glu Thr Glu Trp Phe Phe Phe Phe Ser
 1 5

<210> 17
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 17

Lys Ser Gly Gln Ile Met Val Gly Asn
 1 5

<210> 18
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 18

Arg Cys Phe Tyr
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<210> 19
 <211> 318
 <212> DNA
 <213> mouse

<400> 19
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 agcaatgacg ggaagacctg ggcaatgtac aaagtaaaag gcaccaatga agagatggtc 180
 tttcgtggaa atgttgataa caacacacca tatgctaatt ctttcacacc cccaatcaaa 240
 gctcagtatg taagactcta cccccaatt tgtcgaaggc attgtacttt aagaatggaa 300
 cttcttggct gtgagctc 318

				85					90					95			
Asp	Gly	Xaa	Arg	Lys	Phe	Glu	Phe	Ile	Gln	Asp	Glu	Ser	Gly	Gly	Asp		
			100					105					110				
Lys	Glu	Phe	Leu	Gly	Asn	Leu	Asp	Asn	Asn	Ser	Leu	Lys	Val	Asn	Met		
		115					120					125					
Phe	Asn	Pro	Thr	Leu	Glu	Ala	Gln	Tyr	Ile	Arg	Leu	Tyr	Pro	Val	Ser		
	130					135					140						
Cys	His	Arg	Gly	Cys	Thr	Leu	Arg	Phe	Glu	Leu	Leu	Gly	Cys	Glu	Leu		
145					150					155					160		
His	Gly	Cys	Leu	Glu	Pro	Leu	Gly	Leu	Lys	Asn	Asn	Thr	Ile	Pro	Asp		
			165						170					175			
Ser	Gln	Met	Ser	Ala	Ser	Ser	Ser	Tyr	Lys	Thr	Trp	Asn	Leu	Arg	Ala		
			180					185					190				
Phe	Gly	Trp	Tyr	Pro	His	Leu	Gly	Arg	Leu	Asp	Asn	Gln	Gly	Leu	Ile		
	195						200					205					
Asn	Ala	Trp	Thr	Ala	Gln	Ser	Asn	Ser	Ala	Lys	Glu	Trp	Leu	Gln	Val		
	210					215					220						
Asp	Leu	Gly	Thr	Gln	Arg	Gln	Val	Thr	Gly	Ile	Ile	Thr	Gln	Gly	Ala		
225					230					235					240		
Arg	Asp	Phe	Gly	His	Ile	Gln	Tyr	Val	Glu	Ser	Tyr	Lys	Val	Ala	His		
				245					250					255			
Ser	Asp	Asp	Gly	Val	Gln	Trp	Thr	Val	Tyr	Xaa	Xaa	Glu	Glu	Gln	Gly		
			260					265					270				
Ser	Ser	Lys	Val	Phe	Gln	Gly	Asn	Leu	Asp	Asn	Asn	Ser	His	Lys	Lys		

275

280

285

Asn Ile Phe Glu Lys Pro Phe Met Ala Arg Tyr Val Arg Val Leu Pro
 290 295 300

Val Ser Trp His Asn Arg Ile Thr Leu Arg Leu Glu Leu Leu Gly Cys
 305 310 315 320

<210> 21
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<400> 21

Cys Ser Gly Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln
 1 5 10 15

Ile Thr Ala Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Leu Trp
 20 25 30

Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp
 35 40 45

Thr Ala Ala Glu Asn Asp Arg Trp Asn Arg Trp Ile Gln Ile Asn Leu
 50 55 60

Gln Arg Lys Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg
 65 70 75 80

Ile Gly Ser Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn
 85 90 95

Asp Gly Lys Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Asp
 100 105 110

Met Val Phe Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser
 115 120 125

Phe Thr Pro Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val
 130 135 140

Cys Arg Arg His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu
 145 150 155 160

Ser Gly Cys Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp
 165 170 175

Tyr Gln Ile Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp Met
 180 185 190

Phe Thr Trp Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val
 195 200 205

Asn Ala Trp Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val
 210 215 220

<210> 20
 <211> 320
 <212> PRT
 <213> Homo sapiens

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 <223> Placeholder used in the sequence comparison of SEQ.ID.NOS.20-21

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<220>
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 <222> (267)..(268)
 <223> Placeholder used in the sequence comparison of SEQ.ID.NOS.20-21

<400> 20

Cys Ser Thr Gln Leu Gly Met Glu Gly Gly Ala Ile Ala Asp Ser Gln
 1 5 10 15

Ile Ser Ala Ser Tyr Val Tyr Met Gly Phe Met Gly Leu Gln Arg Trp
 20 25 30

Gly Pro Glu Leu Ala Arg Leu Tyr Arg Thr Gly Ile Val Asn Ala Trp
 35 40 45

His Ala Ser Asn Tyr Asp Xaa Ser Lys Pro Trp Ile Gln Val Asn Leu
 50 55 60

Leu Arg Lys Met Arg Val Ser Gly Val Met Thr Gln Gly Ala Ser Arg
 65 70 75 80

Ala Gly Arg Ala Glu Tyr Leu Lys Thr Phe Lys Val Ala Tyr Ser Leu

Xaa Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala
 225 230 235 240

Lys Asp Xaa Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr
 245 250 255

Ser Asn Asp Gly Glu His Trp Thr Val Xaa Gln Asp Glu Lys Gln Arg
 260 265 270

Lys Asp Lys Val Xaa Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys
 275 280 285

Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro
 290 295 300

Trp Ser Trp Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys
 305 310 315 320

Thr

<210> 22
 <211> 25
 <212> PRT
 <213> Homo sapiens

<400> 22

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly
 1 5 10 15

Val Pro Gln Phe Gly Lys Gly Asp Ile
 20 25

<210> 23
 <211> 57
 <212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (20)..(24)

<223> Placeholder used in the sequence comparison of SEQ.ID.NOS.23-26

<400> 23

Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Pro Gly Leu
1 5 10 15

Ala Val Gly Xaa Xaa Xaa Xaa Xaa Ser Phe Ser Cys Glu Cys Pro Asp
20 25 30

Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Ala Ser Asp
35 40 45

Glu Glu Glu Pro Thr Ser Ala Gly Pro
50 55

<210> 24

<211> 43

<212> PRT

<213> Homo sapiens

<400> 24

Cys Thr Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu
1 5 10 15

Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg
20 25 30

Gly Phe Asn Gly Ile His Cys Gln His Asn Ile
35 40

<210> 25

<211> 42

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (18)..(24)

<223> Placeholder used in the sequence comparison of SEQ.ID.NOS.23-26

<400> 25

Cys	Glu	Val	Glu	Pro	Cys	Lys	Asn	Gly	Gly	Ile	Cys	Thr	Asp	Leu	Val
1				5					10					15	

Ala	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Tyr	Ser	Cys	Glu	Cys	Pro	Gly
			20					25					30		

Glu	Phe	Met	Gly	Arg	Asn	Cys	Glu	Tyr	Lys
		35					40		

<210> 26

<211> 40

<212> PRT

<213> Artificial sequence

<220>

<223> consensus EGF-like domain amino acid sequence

<220>

<221> MISC_FEATURE

<222> (2)..(4)

<223> nonconsensus sequence

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> nonconsensus sequence

<220>

<221> MISC_FEATURE

<222> (11)..(11)

<223> nonconsensus sequence

<220>
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 <222> (13)..(25)
 <223> nonconsensus sequence

<220>
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 <222> (27)..(27)
 <223> nonconsensus sequence

<220>
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 <222> (29)..(29)
 <223> nonconsensus sequence

<220>
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 <222> (31)..(32)
 <223> nonconsensus sequence

<220>
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 <222> (35)..(35)
 <223> nonconsensus sequence

<220>
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 <222> (37)..(38)
 <223> nonconsensus sequence

<220>
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 <222> (40)..(40)
 <223> nonconsensus sequence

<400> 26

Cys	Xaa	Xaa	Xaa	Pro	Cys	Xaa	Asn	Gly	Gly	Xaa	Cys	Xaa	Xaa	Xaa	Xaa
1				5					10					15	

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Cys Xaa Cys Xaa Xaa
 20 25 30

Gly Tyr Xaa Gly Xaa Xaa Cys Xaa
 35 40

<210> 27
 <211> 310
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(1)
 <223> unknown sequence

<400> 27
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 gtaggttcct tttcctgtga gtgtccagat ggcttcacag accccaactg ttctagtgtt 120
 gtggagggttg gtccctgcac tcctaatacca tgccataatg gaggaacctg tgaaataagt 180
 gaagcatacc gaggggatac attcataggc tatgtttgta aatgtcccg aggatttaat 240
 gggattcact gtcagcacia cataaatgaa tgcgaagttg agccttgcaa aaatggtgga 300
 atatgtacag 310

<210> 28
 <211> 2308
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (550)..(1212)
 <223>

<220>
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 <222> (1819)..(1821)
 <223> unknown sequence

<400> 28

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gaattccggg agggagggta ggggggaggc ccgcgggggc ccaaagccag ctaggctcag      60
tctcacacgc gcgccgccac tgtttgtata tagtgcgctc ctggcctcag gctcgctccc      120
ctccagctct cgcttcattg ttctccaagt cagaagcccc cgcatccgcc gcgcagcagc      180
gtgagccgta gtcactgctg gccgcttcgc ctgcgtgcgc gcacggaaat cggggagcca      240
ggaacccaag gagccgccgt ccgcccgtg tgcctctgct agaccactcg cagccccagc      300
ctctctcaag cgcacccacc accactcttt tatcgccctt cccaagattt gagaagcgct      360
atcacccttt ctctagggcc accactcttt tatcgccctt cccaagattt gagaagcgct      420
gcgggaggaa agacgtcctc ttgatctctg acagggcggg gtttactgct gtcctgcagg      480
cgcgctcgc ctactgtgcc ctccgctacg accccggacc agcccaggtc acgtccgtga      540
gaagggatc atg aag cac ttg gta gca gcc tgg ctt ttg gtt gga ctc agc      591
      Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser
            1              5              10

ctc ggg gtg ccc cag ttc ggc aaa ggt gac att tgc aac ccg aac ccc      639
Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro
15              20              25              30

tgt gaa aat ggt ggc atc tgt ctg tca gga ctg gct gat gat tcc ttt      687
Cys Glu Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe
              35              40              45

tcc tgt gag tgt cca gaa ggc ttc gca ggt ccg aac tgc tct agt gtt      735
Ser Cys Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val
              50              55              60

gtg gag gtt gca tca gat gaa gaa aag cct act tca gca ggt ccc tgc      783
Val Glu Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys
              65              70              75

atc cct aac cca tgc cat aac gga gga acc tgt gag ata agc gaa gcc      831
Ile Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala
              80              85              90

tat cga gga gac aca ttc ata ggc tat gtt tgt aaa tgt cct cgg gga      879
Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly
95              100              105              110

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ttt aat ggg att cac tgt cag cac aat ata aat gaa tgt gaa gct gag	927
Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu	
115 120 125	
cct tgc aga aat ggc gga ata tgt acc gac ctt gtt gct aac tac tct	975
Pro Cys Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser	
130 135 140	
tgt gaa tgc cca gga gaa ttt atg gga cga aat tgt caa tat aaa tgc	1023
Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys	
145 150 155	
tct ggg cac ttg gga atc gaa ggt ggg atc ata tct aat cag caa atc	1071
Ser Gly His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile	
160 165 170	
aca gct tca tct aat cac cga gct ctt ttt gga ctc cag aag tgg tat	1119
Thr Ala Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr	
175 180 185 190	
ccc tac tat gct aga ctt aat aag aag ggc ctt ata aat gcc tgg aca	1167
Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr	
195 200 205	
gct gct gaa aat gac aga tgg cca tgg att cag gta aca gtg gga	1212
Ala Ala Glu Asn Asp Arg Trp Pro Trp Ile Gln Val Thr Val Gly	
210 215 220	
tgagacaaat ccatttccca aattatcaga atcattatag aagtaggtta gggagaattg	1272
gctgtgattc tttctcatgg ttaaaatgtg atttagttca gaattaacat gggttgaaac	1332
tctaaaaaat gtggaaaaca ggaacattct atgtctgaaa atctgaaaat agcatcaaga	1392
tgaaaacatt ctttagtcat aaatatactc ttttaagtta tagtagagaa aaagatctta	1452
tcatttcata agtggacttt tgggatagca ttggaaatgt aaatgaaata aataccta	1512
tgaaaaaagt ttattctaaa gtgttaatat ttagcaacag attcagagac aagaaagtaa	1572
caattcaatc tgtgtathtt ttgtgagaaa tagtttccca tgtgcaaata taaagtgcgc	1632
atcatatcat gataatatcc aactgtctgc agaactccct ttcataaatg agagaathtt	1692
aattcatagt gccttatatc ctcatcagcc atctgacttt actacagaag aaaacaatga	1752
aatgatgcat taagtgcttt gctagaagaa acatcatagc aaagctgata gccacattc	1812

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tgtgcannna agcttccaga gcactcgaga aaaagcagaa atgagatggt ttatgaaaac 1872
cgaaaagata atctgatttc tgtgaaatat acttttgatc atgtgggttct ttaagatagt 1932
cactaacaag tcattagtag cagataccaa atgggagaaa atttccagta tactgagggt 1992
caaggcagtc atgctgaaac tacatgaggt caggaaagtt ttgaaataag gtgattttgg 2052
aaggatacct tcaactggcc tagattttca agaaacagtg taatcaacag ccaaacatga 2112
gaatctagct aacagcattt agaaaaccag aactaagagt gttactgggg aattgcattt 2172
aatccagta tgagagtttg caaatgccgt attcttctaa ggggtttgtg ccacattttg 2232
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ataaaagccg gaattc 2308

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<210> 29
<211> 221
<212> PRT
<213> mouse

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<220>
<221> misc_feature
<222> (1819)..(1821)
<223> unknown sequence

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<400> 29

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Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser Leu Gly
1           5           10           15

```

```

Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro Cys Glu
          20           25           30

```

```

Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe Ser Cys
    35           40           45

```

```

Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val Val Glu
    50           55           60

```

Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys Ile Pro
65 70 75 80

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
85 90 95

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
100 105 110

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu Pro Cys
115 120 125

Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
130 135 140

Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
145 150 155 160

His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
165 170 175

Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
180 185 190

Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
195 200 205

Glu Asn Asp Arg Trp Pro Trp Ile Gln Val Thr Val Gly
210 215 220

<210> 30

<211> 481

<212> PRT

<213> Homo sapiens

<400> 30

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly

1

5

10

15

Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu
 20 25 30

Asn Gly Gly Ile Cys Leu Pro Gly Leu Ala Val Gly Ser Phe Ser Cys
 35 40 45

Glu Cys Pro Asp Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu
 50 55 60

Val Ala Ser Asp Glu Glu Glu Pro Thr Ser Ala Gly Pro Cys Thr Pro
 65 70 75 80

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
 85 90 95

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
 100 105 110

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys
 115 120 125

Lys Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
 130 135 140

Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
 145 150 155 160

Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
 165 170 175

Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
 180 185 190

Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala

195

200

205

Glu Asn Asp Arg Trp Lys Arg Trp Ile Gln Ile Asn Leu Gln Arg Lys
 210 215 220

Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser
 225 230 235 240

Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys
 245 250 255

Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Asp Met Val Phe
 260 265 270

Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro
 275 280 285

Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val Cys Arg Arg
 290 295 300

His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys
 305 310 315 320

Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile
 325 330 335

Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp
 340 345 350

Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp
 355 360 365

Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu
 370 375 380

Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe

Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Gly Pro Cys Thr Pro
35 40 45

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
50 55 60

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
65 70 75 80

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys
85 90 95

Lys Asn Gly Gly Ile Cys Thr
100